IFW16

RAW SEQUENCE LISTING   DATE: 07/27/2004
PATENT APPLICATION: **US/09/145,916E**   TIME: 16:16:53

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\07272004\I145916E.raw**

SEQUENCE LISTING
```
 1 (1)  GENERAL INFORMATION:
 2      (i)  APPLICANT: Simons, Michael
 3                      Volk, Rudiger
 4                      Horowitz, Arie
 5     (ii)  TITLE OF INVENTION: Stimulation of angiogenesis
 6                               via enhanced endothelial expression of syndecan-4
 7                               core proteins
 8    (iii)  NUMBER OF SEQUENCES: 25
 9     (iv)  CORRESPONDENCE ADDRESS:
10           (A) ADDRESSEE: David Prashker, Esq.
11           (B) STREET: P.O. Box 5387
12           (C) CITY: Magnolia
13           (D) STATE: Massachusetts
14           (E) COUNTRY: USA
15           (F) ZIP: 01930
16      (v)  COMPUTER READABLE FORM:
17           (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
18           (B) COMPUTER: Dell PC
19           (C) OPERATING SYSTEM: MS DOS
20           (D) SOFTWARE: Microsoft Word version 97
21     (vi)  CURRENT APPLICATION DATA:
C--> 22           (A) APPLICATION NUMBER: US/09/145,916E
C--> 23           (B) FILING DATE: 02-Sep-1998
24           (C) CLASSIFICATION: Unknown
25   (viii)  ATTORNEY/AGENT INFORMATION:
26           (A) NAME: David Prashker, Esq.
27           (B) REGISTRATION NUMBER: 29,693
28           (C) REFERENCE/DOCKET NUMBER: BIS-039
29     (ix)  TELECOMMUNICATION INFORMATION:
30           (A) TELEPHONE: (978) 525-3794
31 (2)  INFORMATION FOR SEQ ID NO: 1:
32      (i)  SEQUENCE CHARACTERISTICS:
33           (A) LENGTH: 762 base pairs
34           (B) TYPE: nucleic acid
35           (C) STRANDEDNESS: single
36           (D) TOPOLOGY: linear
37     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
39 ATGAGACGTG CGGCGCTCTG GCTTTGGCTC TGCGCGCTGG CGCTGCGCCT GCAGCCTGCC 60
40 CTCCCGCAAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC 120
41 TCAGACAACT CTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180
42 ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240
43 ACCAGCAGGG ATACCGAGGC CACCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300
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44 GAGGGAGAGC CCGTGGCCCA CGTGGAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360
45 AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCTCA 420
46 ACAGCAGCCA GAGCCACCAC GGCCCAGGCA TCTGTCACGT CTCATCCCCA CGGGGATGTG 480
47 CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540
48 CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAAACTACC 600
49 AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTTGA AACATCTGGG 660
50 GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720
51 GGAGCCACAG GTGCTTCTCA GGGCCTTTTG GACAGGAAGG AA                 762
53 (2) INFORMATION FOR SEQ ID NO: 2:
54     (i) SEQUENCE CHARACTERISTICS:
55         (A) LENGTH: 1020 base pairs
56         (B) TYPE: nucleic acid
57         (C) STRANDEDNESS: single
58         (D) TOPOLOGY: linear
59     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
61 GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60
62 GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC 120
63 GCTGCTCTCC AGATACCCCC GGAGCTCCAG CCGCGCGGAT CGCGCGCTCC CGCCGCTCTG 180
64 CCCCTAAACT TCTGCCGTAG CTCCCTTTCA AGCCAGCGAA TTTATTCCTT AAAACCAGAA 240
65 ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300
66 AGCTTCAGAG AGCAGCCTTC CCGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360
67 AGTGAGAGGG CGCCGCGTTC CCGGGGCGCA GCTGCGGGCG CGGGAGCAG GCGCAGGAGG 420
68 AGGAAGCGAG CGCCCCCGAG CCCCGAGCCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480
69 GGTACTCTGC TCCGGATTCG TGTGCGCGGG CTCGCCGAGC GCTGGGCAGG AGGCTTCGTT 540
70 TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGGAATAT GCGGCGCGCG 600
71 TGGATCCTGC TCACCTTGGG CTTGGTGGCC TGCGTGTCGG CGGAGTCGAG AGCAGAGCTG 660
72 ACATCTGATA AAGACATGTA CCTTGACAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
73 CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780
74 AGTCCAGAGC TGACAACAAC TCGACCACTT CCAAAGATAC TGTTGACTAG TGCTGCTCCA 840
75 AAAGTGGAAA CCACGACGCT GAATATACAG AACAAGATAC CTGCTCAGAC AAAGTCACCT 900
76 GAAGAAACTG ATAAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960
77 GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTTAA ACGGACAGAA 1020
79 (2) INFORMATION FOR SEQ ID NO: 3:
80     (i) SEQUENCE CHARACTERISTICS:
81         (A) LENGTH: 340 amino acids
82         (B) TYPE: amino acid
83         (C) STRANDEDNESS: single
84         (D) TOPOLOGY: linear
85     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
87 Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Glu Lys Glu Glu
88 1             5               10                15
89 Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala
90             20              25              30
91 Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu
92         35              40              45
93 Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe
94     50              55              60
95 Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu
96 65              70              75              80
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 97 Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln
 98                 85                   90                   95
 99 Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser
100                100                  105                  110
101 Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
102             115                  120                  125
103 Gly Ala Ala Ala Gly Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
104         130                  135                  140
105 Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
106 145                  150                  155                  160
107 Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
108                 165                  170                  175
109 Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Ala Gly Ser Ser Arg
110                 180                  185                  190
111 Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
112             195                  200                  205
113 Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
114         210                  215                  220
115 Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
116 225                  230                  235                  240
117 Pro Ile Asp Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
118                 245                  250                  255
119 Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
120             260                  265                  270
121 Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Thr Leu Asn
122         275                  280                  285
123 Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp
124         290                  295                  300
125 Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
126 305                  310                  315                  320
127 Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
128             325                  330                  335
129 Lys Arg Thr Glu
130             340
132 (2) INFORMATION FOR SEQ ID NO: 4:
133      (i) SEQUENCE CHARACTERISTICS:
134          (A) LENGTH: 1079 base pairs
135          (B) TYPE: nucleic acid
136          (C) STRANDEDNESS: single
137          (D) TOPOLOGY: linear
138      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
140 GCCCCCGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCCCGCGGAG CTGCGGCGCC 60
141 TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
142 AGAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180
143 ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
144 TGGAGACAGC GGTCAGCCTC ACCACGGACA CGTCCGTCCC ACTGCCCACC ACGGTGGCCG 300
145 TGCTGCCTGT CACCTTGGTG CAGCCCATGG CAACACCCTT TGAGCTGTTC CCCACAGAGG 360
146 ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAG 420
147 TGATCCCCAG CTGGAAAACA ACCACCGCCA GTACCACTGC CAGTGACTCC CCCAGTACCA 480
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148 CCTCCACCAC CACCACCACG GCTGCTACCA CCACCACAAC CACCACCACC ATCAGCACCA 540
149 CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCCT GCCCCCCTTT GTCACCAAGG 600
150 CAGCCACCAC CCGGGCCACC ACCCTGGAGA CGCCCACCAC CTCCATCCCT GAAACCAGTG 660
151 TCCTGACAGA GGTGACCACA TCACGGCTTG TCCCCTCCAG CACAGCCAAG CCGAGGTCCC 720
152 TGCCAAAACC AAGCACTTCC AGGACTGCAG AACCCACGGA AAAAAGCACT GCCTTGCCTT 780
153 CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
154 CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTCGAGA 900
155 TCCAGGAGGA GGAGGAGACA ACTCGTCCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960
156 CACCACCAGC AGCACCGGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
157 TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA  1079
159 (2) INFORMATION FOR SEQ ID NO: 5:
160      (i) SEQUENCE CHARACTERISTICS:
161           (A) LENGTH: 447 base pairs
162           (B) TYPE: nucleic acid
163           (C) STRANDEDNESS: single
164           (D) TOPOLOGY: linear
165      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
167 ATGGCGCCTG TCTGCCTGTT TGCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
168 GCCCCAGGCG AGTCGATTCG AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
169 AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCTTGA GCAGGACTCT 180
170 GACTTTGAGC TGTCGGGTTC CGGAGATCTA GATGACACGG AGGAGCCCAG GACCTTCCCT 240
171 GAGGTGATTT CACCCTTGGT GCCACTAGAT AACCACATCC CCGAGAATGC CCAGCCTGGC 300
172 ATCCGTGTCC CCTCAGAGCC CAAGGAACTG GAAGAGAATG AGGTCATTCC CAAAAGGGTC 360
173 CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCCAG 420
174 GGCAGCAACA TTTTTGAAAG AACTGAG                                    447
176 (2) INFORMATION FOR SEQ ID NO: 6:
177      (i) SEQUENCE CHARACTERISTICS:
178           (A) LENGTH: 1590 base pairs
179           (B) TYPE: nucleic acid
180           (C) STRANDEDNESS: single
181           (D) TOPOLOGY: linear
182      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
184 ATGGAGCTCC GGGCCCGAGG CTGGTGGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
185 GCCCGCGGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCCA GATCTACGGG 120
186 GCTAAGGGCT TTAGCCTGAG CGACGTGCCC CAGGCAGAGA TCTCGGGAGA GCACCTGCGG 180
187 ATCTGCCCCC AGGGCTACAC CTGCTGCACC AGTGAGATGG AGGAGAACCT GGCCAACCAC 240
188 AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
189 GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGCGCC TGCTGAATGA CTCGGAGCGT 360
190 ACACTGCAGG ATGCTTTTCC CGGGGCCTTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
191 TTCCGGGACC TGTATGCTGA GCTGCGTCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
192 GAGACACTGG CCGAGTTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540
193 CAGCTTCTGC TGCCCGATGA CTATCTGGAC TGCCTGGGCA AGCAGGCAGA GGCACTGCGG 600
194 CCGTTTGGGG ATGCCCCTCG AGAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
195 CGATCCTTTG TGCAGGGCCT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCCAGGTT 720
196 CCTCTGGCCC CAGAATGTTC TCGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATTGCCGG 780
197 GGAGTCCCTG GTGCCCGGCC CTGTCCCGAC TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
198 GCCAACCAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
199 ACTGACAAGT TCTGGGGCCC GTCGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
200 CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAGGACA CACTCACAGC TAAGGTCATC 1020
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            Input Set : A:\PTO.FG.txt
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201 CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
202 CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAAAA GCTGGTCTCT 1140
203 GAGGCCAAGG CCCAGCTCCG AGACATTCAG GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
204 TGTAGTGAGA AGATGGCCAT GAGTCCTGCC AGCGATGACC GCTGCTGGAA TGGGATTTCC 1260
205 AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCCT 1320
206 GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
207 AAGATCATGA CCAACCGTTT ACGTGGCGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440
208 GCCAGTGATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
209 CGGAGGGTCA GCAAGAAGAG CTCCAGCTCC CGGACCCCCT TGACCCATGC CCTCCCCGGC 1560
210 TTGTCAGAAC AGGAGGGACA GAAGACCTCG   1590
212 (2) INFORMATION FOR SEQ ID NO: 7:
213   (i) SEQUENCE CHARACTERISTICS:
214   (A) LENGTH: 531 amino acids
215   (B) TYPE: amino acid
216   (C) STRANDEDNESS: single
217   (D) TOPOLOGY: linear
218   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
220 Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
221 1   5   10   15
222 Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
223   20   25   30
224 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
225   35   40   45
226 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
227   50   55   60
228 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His
229 65   70   75   80
230 Ser Arg Met Glu Leu Glu Thr Ala Leu His Asp Ser Ser Arg Ala Leu
231   85   90   95
232 Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln
233   100   105   110
234 Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Asp Ala Phe Pro Gly
235   115   120   125
236 Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu
237   130   135   140
238 Tyr Ala Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu
239 145   150   155   160
240 Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys
241   165   170   175
242 Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu
243   180   185   190
244 Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu
245   195   200   205
246 Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val
247   210   215   220
248 Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val
249 225   230   235   240
250 Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys
251   245   250   255

VERIFICATION SUMMARY   DATE: 07/27/2004
PATENT APPLICATION: **US/09/145,916E**   TIME: 16:16:54

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L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]